

Plant Gene Register

A *Zea mays* Pollen cDNA Encoding a Putative Actin-Depolymerizing Factor¹

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Microfilaments perform essential functions in eukaryotic cells, being responsible, in conjunction with other cytoskeletal elements, for the structural integrity of the cell and also for many of the cellular movements, including muscle contraction, cytokinesis, cytoplasmic streaming, and phagocytosis. The structural versatility of microfilaments is mediated by actin-binding proteins (Hartwig and Kwiatkowski, 1991). A group of small actin-binding proteins, the ADF group, has the ability to regulate actin polymerization and depolymerization. Proteins within the ADF group have similar properties and they include vertebrate ADF (Bamburg et al., 1980), or destrin (Moriyama et al., 1990), vertebrate and yeast cofilin (Nishida et al., 1984; Iida et al., 1993), starfish depactin (Mabuchi, 1981), and *Acanthamoeba* actophorin (Cooper et al., 1986). Chemical cross-linking experiments, mutational analysis, and competition studies using synthetic peptides have demonstrated that the amino acid region from Trp¹⁰⁴ to Leu¹²⁸ in pig cofilin is likely to be a multifunctional domain binding both phosphoinositides and actin (Yonezawa et al., 1991a, 1991b; Moriyama et al., 1992); the Lys¹¹⁴ plays a pivotal role in the actin-depolymerizing activity of cofilin (Moriyama et al., 1992). This amino acid region is highly conserved among the members of the ADF group.

Recently, a lily anther preferentially expressed cDNA was isolated and sequenced by An and colleagues (Kim et al., 1993), and the deduced amino acid sequence showed significant homology to the proteins in the ADF group. In a similar study, we differentially screened a maize pollen cDNA library with radiolabeled shoot and pollen cDNA and isolated a pollen-abundant cDNA, *ZmABP1*. The nucleotide sequence of *ZmABP1* shows homology to the lily cDNA and to the members of the ADF group (Table I).

ZmABP1 was found to encode a protein of 139 amino acids. The deduced amino acid sequence shows 70% identity (97% similarity) with the lily sequence. A comparison of the maize sequence with the sequence of the members of

Table I. Characteristics of a cDNA encoding a putative ADF from *Zea mays*

Organism:	<i>Zea mays</i> , inbred line A188.
Clone Type:	cDNA, full-length.
Source:	cDNA library in Bluescribe M13+, constructed from maize (A188) pollen poly(A) ⁺ RNA.
Techniques:	60,000 colonies of the pollen cDNA library were hybridized sequentially with radiolabeled shoot and pollen first-strand cDNA. Colonies showing a differential hybridization with the shoot and pollen cDNA were isolated. The <i>ZmABP1</i> clone was isolated as a pollen-abundant clone and was completely sequenced using dideoxy sequencing.
Sequence Comparison:	All comparisons were carried out using the Bestfit program in the Genetics Computer Group Sequence Analysis software package. The nucleotide and deduced amino acid sequence showed significant homology to the putative lily ADF sequence and to the sequences of the different members of the ADF group.
Structural Features of the Protein:	The open reading frame encodes 139 amino acids with a predicted molecular mass of 16,167 D and a pI of 5.42. A putative actin and phospholipid-binding domain resides between Trp ⁹⁰ and Leu ¹¹⁴ .

the ADF group reveals that most homology is exhibited with yeast cofilin (44% identity, 83% similarity) and least homology with starfish depactin (22% identity, 72% similarity). In addition, the pig cofilin actin and phosphoinositide-binding domain (Trp¹⁰⁴-Leu¹²⁸) shows 52% identity (96% similarity) with the corresponding maize sequence (Trp⁹⁰-Leu¹¹⁴). Although the biological activity of the *ZmABP1* protein has yet to be determined, the sequence comparisons suggest that the protein will have actin-binding properties.

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The EMBL accession number for the sequence reported in this article is X80820.

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Abbreviation: ADF, actin-depolymerizing factor.

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